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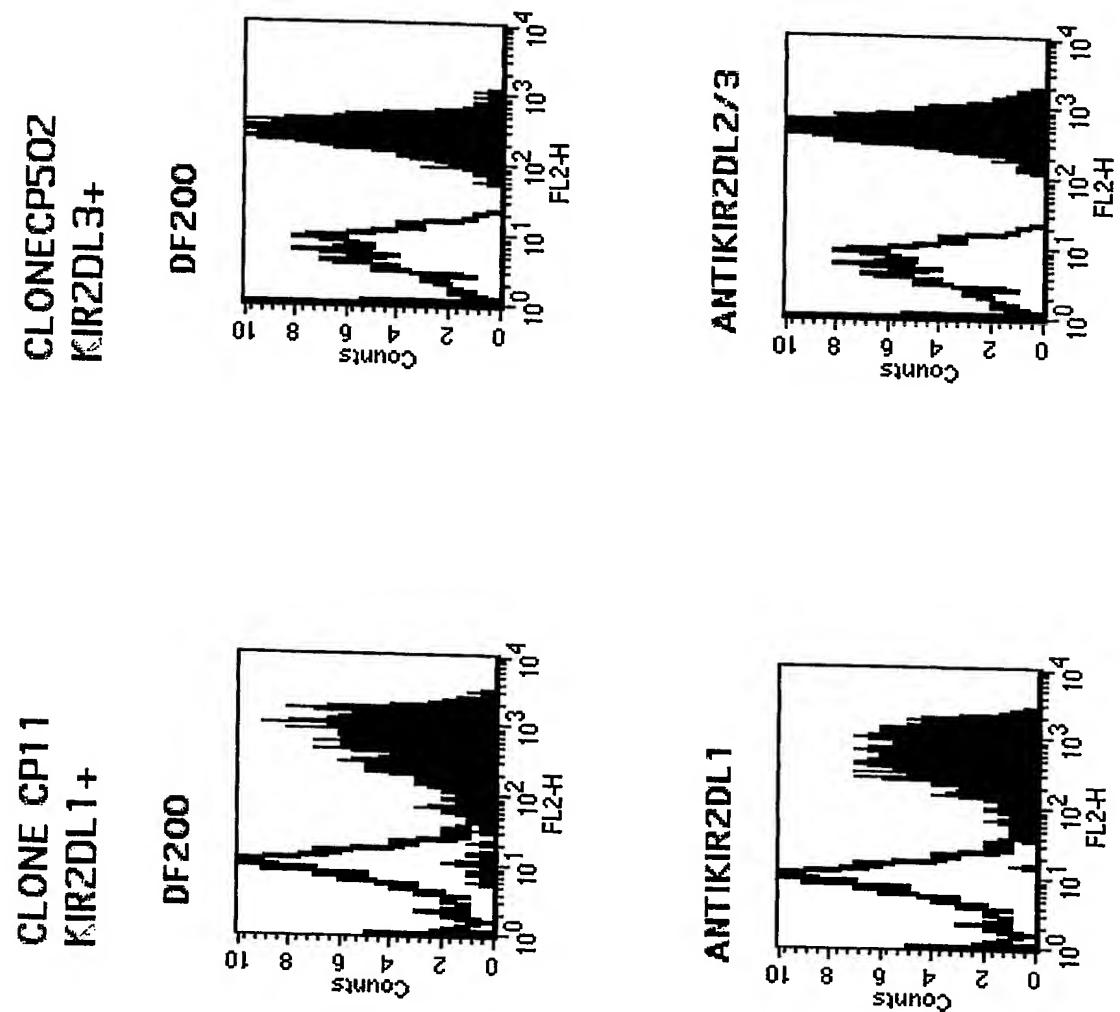
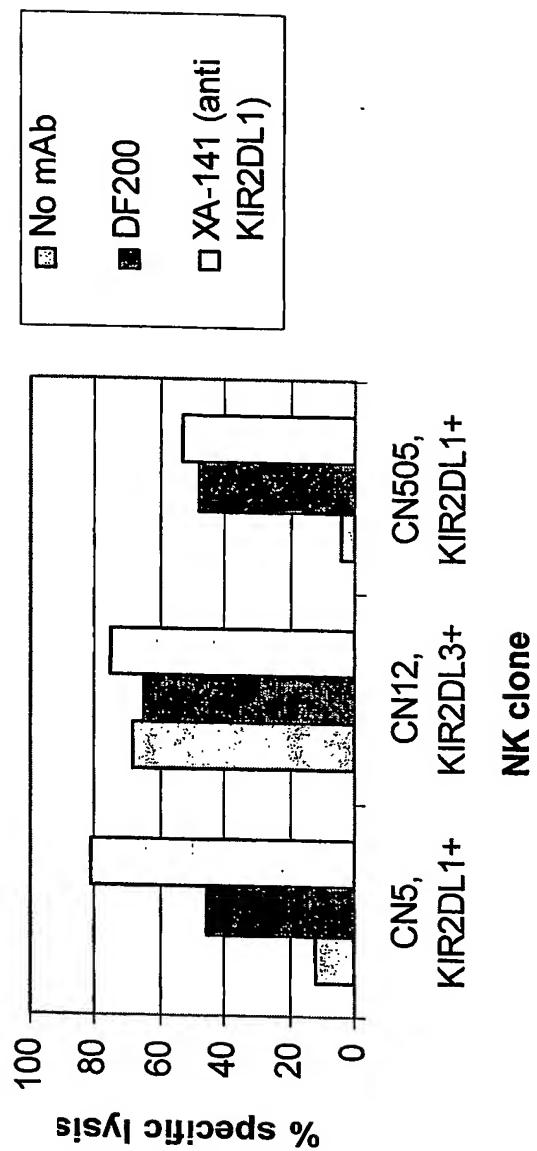


FIG 1

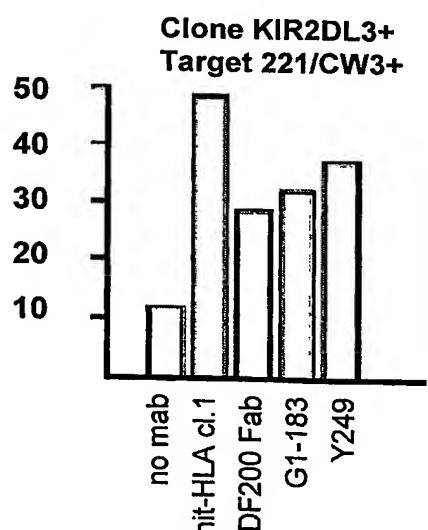
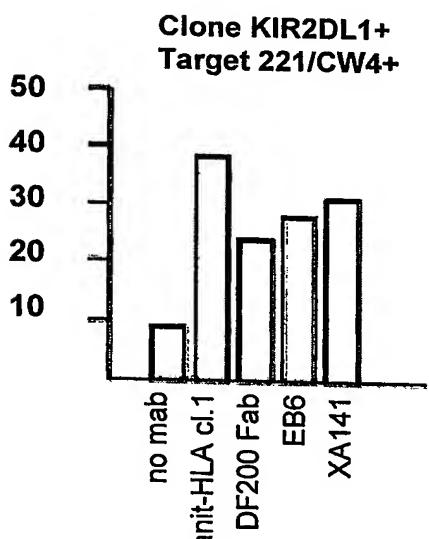
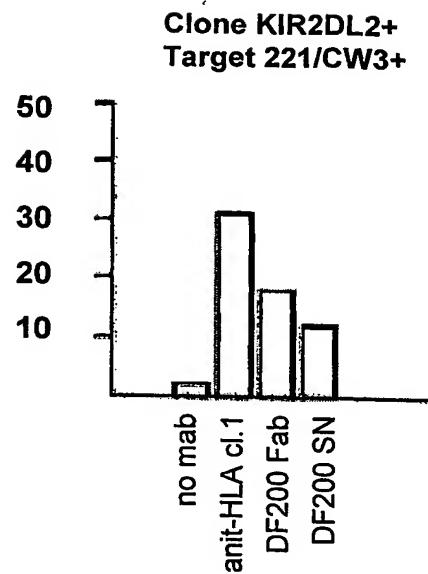
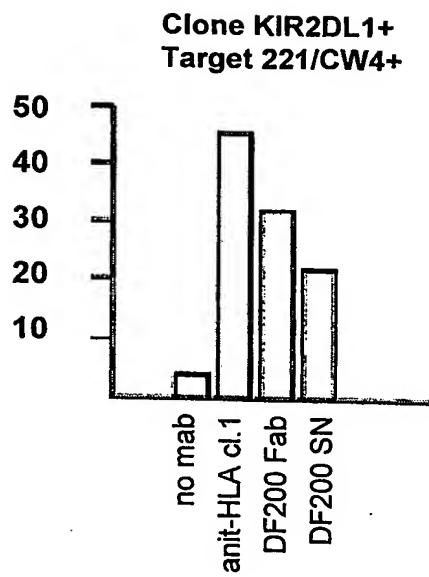
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**Reconstitution of lysis with anti KIR2D mAb on C1R**  
**Cw4 target at effector /target ratio of 4/1**



**FIG 2**

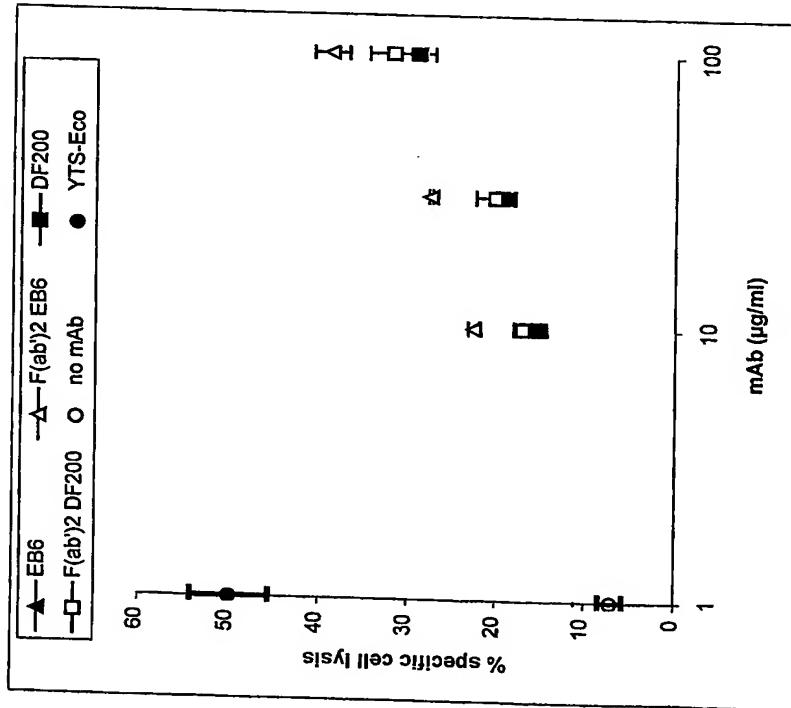
Rest Available Copy

**FIG 3**

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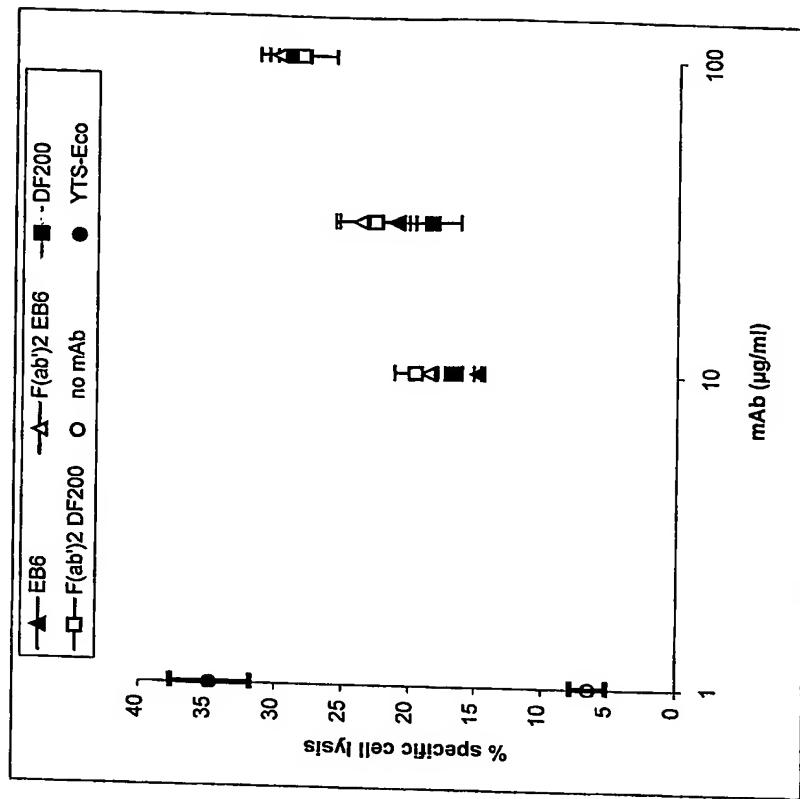
FIG 4

Target cell: FIG 4A : 721.221-cw4



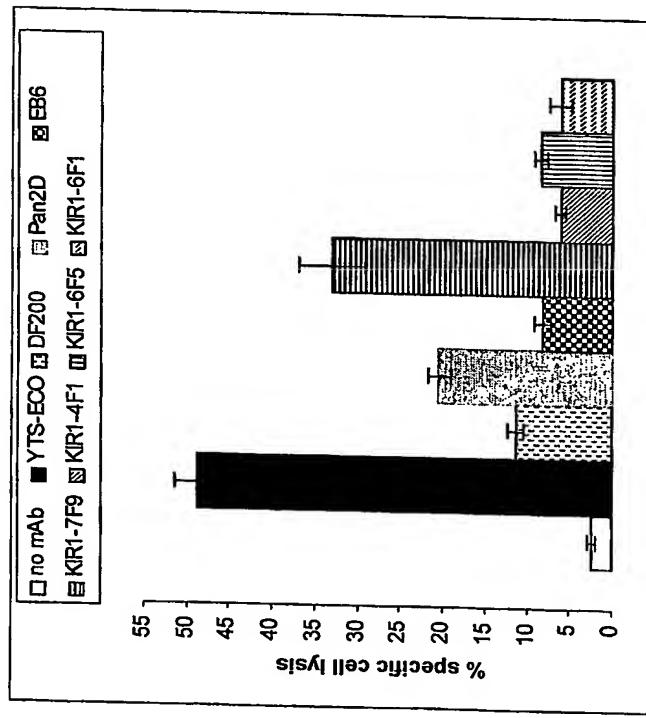
E/T ratio= 1

FIG 4B : TUBO

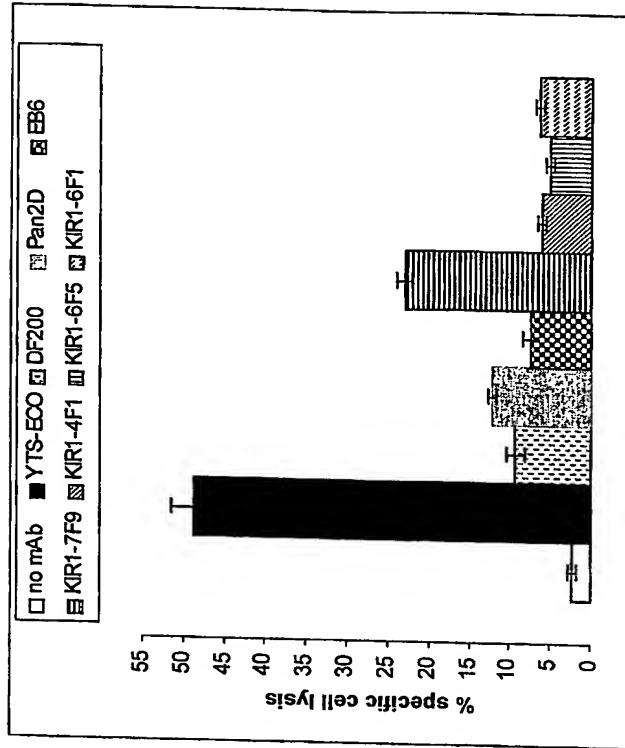


E/T ratio= 2

FIG 5

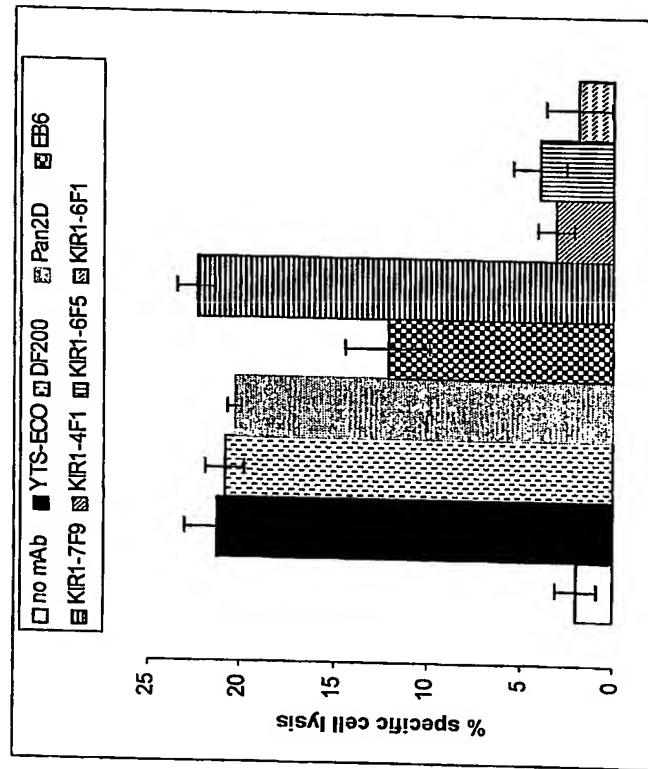
FIG 5A : mAb: 30 $\mu$ g/ml

E/T ratio= 1

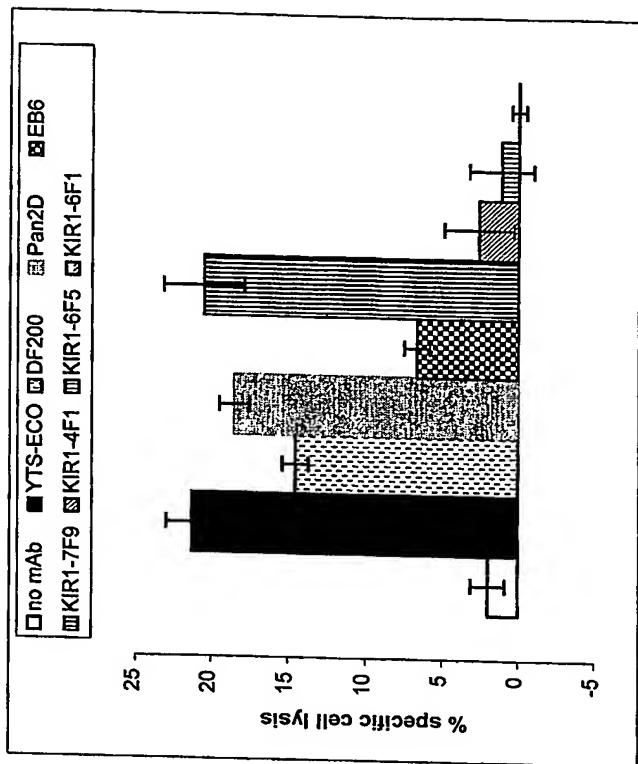
FIG 5B : mAb: 10 $\mu$ g/ml

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FIG 6

FIG 6A: mAb: 30 $\mu$ g/ml

E/T ratio= 2

FIG 6B : mAb: 10 $\mu$ g/ml

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FIG 7

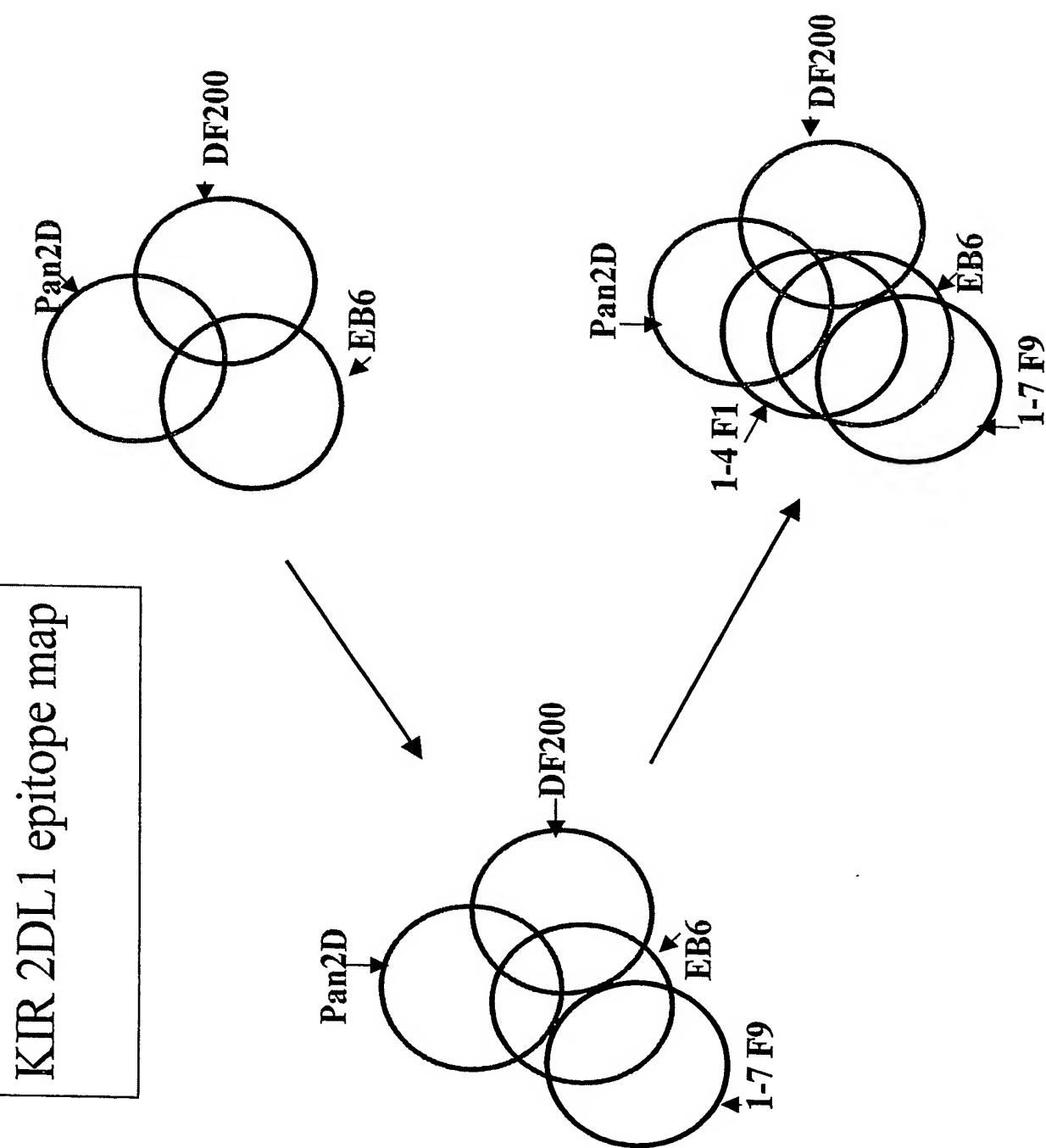
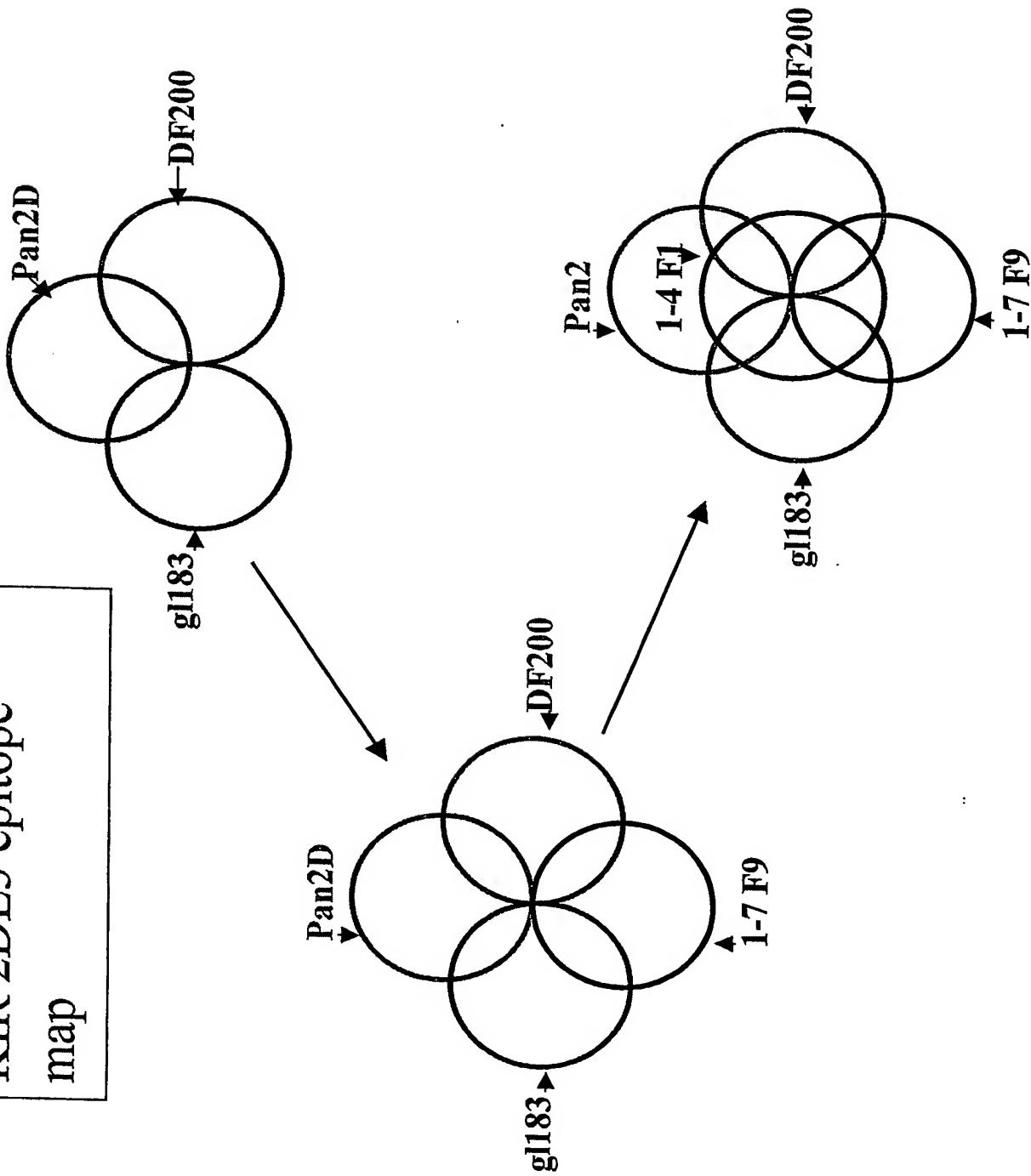
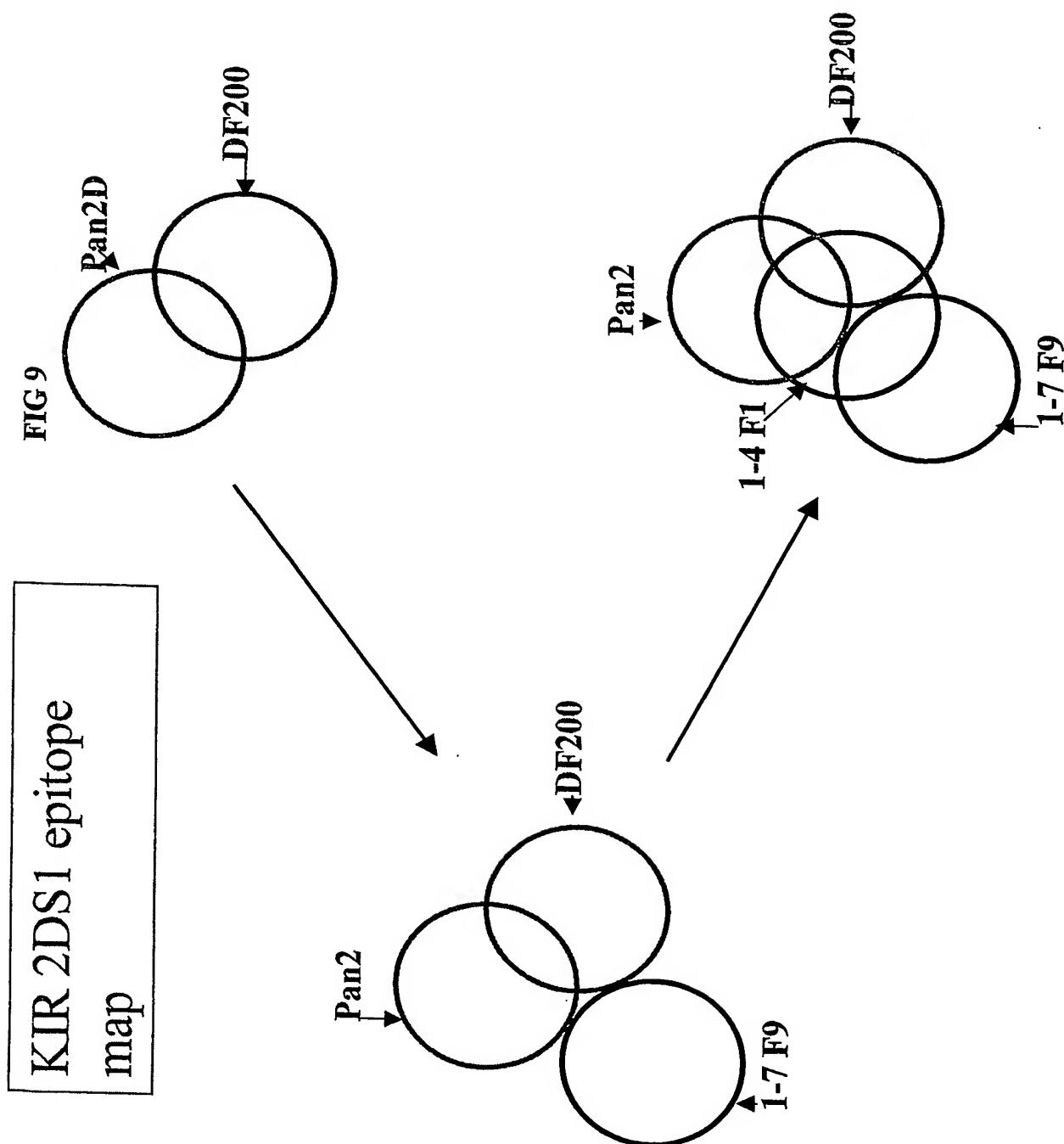


FIG 8

KIR 2DL3 epitope  
map



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FIG 10

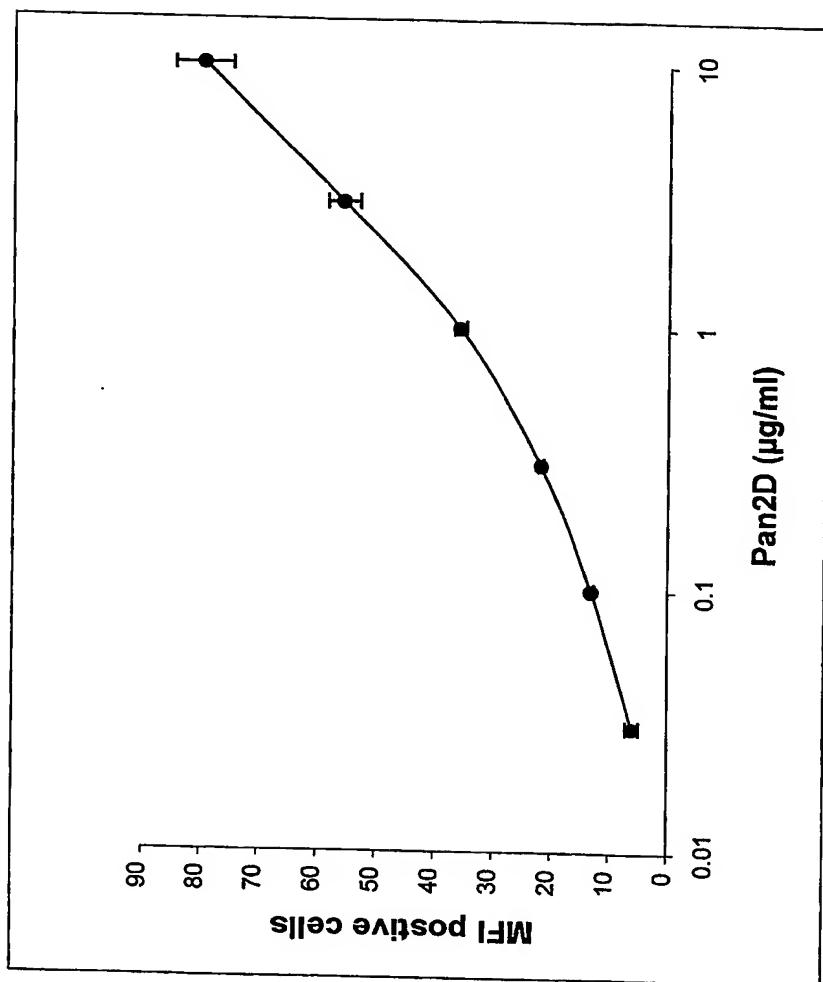
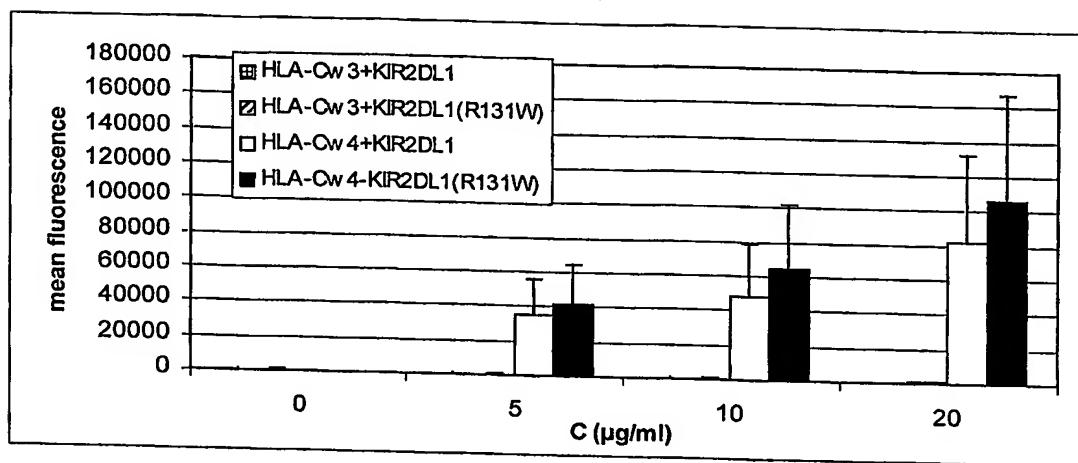
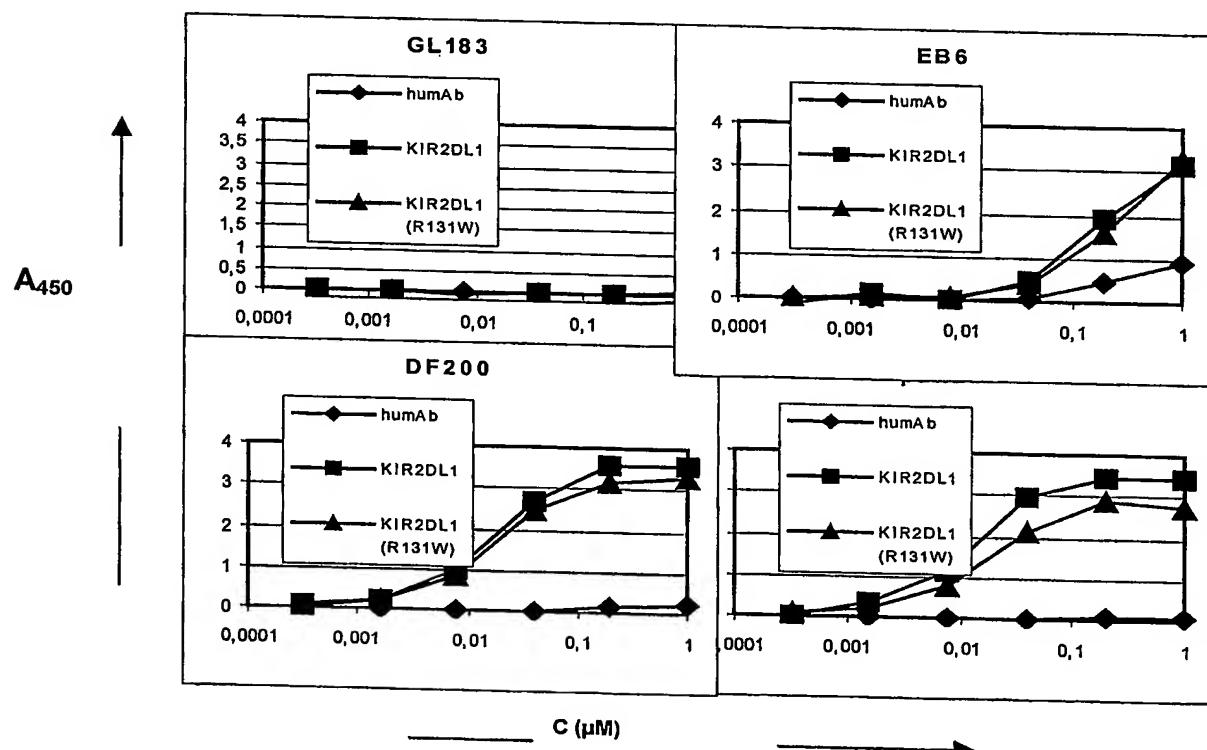


FIG 11

## FIG 11A KIR2DL1(R131W)-hFc



## FIG 11B



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## Anti-KIR light variable regions

DF-200 light variable	(1)	M--ESOTLVE <u>S</u> ILLW <u>T</u> YGD <u>G</u> NNIV <u>T</u> OSPKSMS <u>T</u> IGERV <u>T</u> ITCKASEN	50
PAN2D-Light-variable	(1)	MDFQVQIFSE <u>L</u> ISASW <u>M</u> SRG <u>G</u> IV <u>T</u> OSBASMS <u>A</u> IGERV <u>T</u> ITCTASSS	
Consensus	(1)	Q F I I L A GNIVLTQSP SMS SIGERVLTCA	
	51		
DF-200 light variable	(49)	V <u>V</u> I-Y <u>W</u> SW <u>Y</u> Q <u>Q</u> KPE <u>Q</u> SP <u>K</u> L <u>I</u> Y <u>G</u> AS <u>N</u> RY <u>T</u> G <u>P</u> D <u>E</u> F <u>T</u> G <u>S</u> A <u>T</u> D <u>E</u> LT <u>I</u> SS	100
PAN2D-Light-variable	(51)	V <u>S</u> SS <u>X</u> W <u>Y</u> Q <u>Q</u> K <u>P</u> G <u>S</u> S <u>P</u> R <u>I</u> W <u>T</u> Y <u>T</u> S <u>N</u> L <u>A</u> S <u>G</u> V <u>P</u> A <u>R</u> E <u>S</u> G <u>S</u> G <u>T</u> S <u>N</u> L <u>I</u> SS	
Consensus	(51)	V S YL WYQQKP SPKL IY SN SGVP RFSGSGSAT FSLTISS	
	101		
DF-200 light variable	(98)	Y <u>Q</u> A <u>E</u> D <u>L</u> A <u>D</u> Y <u>H</u> G <u>Q</u> G <u>S</u> Y <u>P</u> T <u>F</u> GG <u>G</u> T <u>K</u> L <u>E</u> I <u>K</u> R	131
PAN2D-Light-variable	(101)	M <u>E</u> A <u>E</u> D <u>A</u> T <u>T</u> Y <u>H</u> Q <u>Y</u> Y <u>R</u> S <u>P</u> P <u>T</u> F <u>GG</u> G <u>G</u> T <u>K</u> L <u>E</u> I <u>K</u> R	
Consensus	(101)	M AED A YHC Q H P T FGGGTKEIKR	

Numbers above amino acid sequences indicate position respective to initiation of translation Met (+1) in the immature (non-secreted) immunoglobulin. Underlined are the CDR regions

## CDR's from the anti-KIR light variable regions

## CDR-L1 from clones PAN-2D and DF-200

Residue before: Normally Cys. Residues after: Trp. Typically Trp-Tyr-Leu. Length: 10-17 aa  
Start: approximately 24 aa from the beginning of secreted protein

DF-200 light variable	(44)	KASEN <u>V</u> V <u>T</u> -Y <u>S</u>	(70)	GASNR <u>T</u>
PAN2D-Light-variable	(46)	TASSSS <u>V</u> S <u>T</u> Y	(73)	STS <u>N</u> L <u>A</u> S
Consensus		AS V S YL		SN S

## CDR-L3 from clones PAN-2D and DF-200

Residues before: Cys  
Residues after: Phe-Gly-XXX-Gly

Length: 7-11 aa  
Start: approximately 33 aa after the end of CDR-L2  
DF-200 light variable (109) GQQGSYPT  
PAN2D-Light-variable (112) HQZHRSPT  
Consensus Q H P T

## CDR-L2 from clones PAN-2D and DF-200

Residues before: Generally Ile-Tyr  
Length: 7 aa  
Start: approximately 16 aa after the end of CDR-L1

DF-200 light variable	(70)	GASNR <u>T</u>
PAN2D-Light-variable	(73)	STS <u>N</u> L <u>A</u> S
Consensus		SN S

FIG 13

>DF-200VH\immature-PROT  
 MAVLGILLFCLVTFPSCVLS  
 QVQLEQSGPGGLVQPSQSLISITCTVSGFSFTPYGVHWWVRQSPGKGLEWLTGYIWSGGNTDYNAAFISRLSINKDNSKSSQVFFKMNNSIQLVND  
 TAIYYCARNPRPGNYPYGMIDYWQGGTSVTVSS

### Anti-KIR heavy variable regions (immature Fabs)

Sequences including CDR regions in heavy variable regions	
<b>CDR-H1 from clone DF-200</b> Residues before: Cys-XXX-XXX-XXX Residues after: Trp. Generally Trp-Val or Trp-Ile Length: 10-14 aa Start: Approximately 22-26 aa from the beginning of the secreted protein GFSFTPYGVH	<b>CDR-H2 from clone DF-200</b> Residues before: Leu-Glu-Trp-Ile-Gly but other variations possible Residues after: Lys or Arg / Leu or Ile or Val or Phe or Thr or Ala / Thr or Ser or Ile or Ala Length: 16-20 aa Start: Approximately 15 aa after the end of CDR-H1 VTWSGGNTDYNAAFIS
<b>CDR-H3 from clones 4G1, 5D5 and 6C12</b> Residues before: Cys-XXX-XXX (Typically Cys-Ala-Arg) Residues after: Trp-Gly-XXX-Gly Length: 3-25 aa Start: Approximately 33 after the end of CDR-H2 NPPRPGNYPYGMIDY	

The secreted, mature VH starts at:  
 Position 20: residue Q

The VH region ends with residue S and thereafter the constant region (not shown) continues